

On page 7, please delete the paragraph at lines 23-26 and replace it with the following paragraph:

Figure 2 depicts a summary of the alignment of the human MEKK1 protein (SEQ ID NO:2) with a partial human MEKK1 protein (GenBank Accession Number AF042838), (SEQ ID NO:3) rat MEKK1 (GenBank Accession Number U48596) (SEQ ID NO:4) , and mouse MEKK1 (GenBank Accession Number AF117340.1) (SEQ ID NO:5).

On page 23, please delete the subparagraphs at lines 12-27 and replace them with the following subparagraphs:

a nucleic acid molecule comprising from about 10 to about 64 contiguous nucleotides from the nucleic acid sequence (SEQ ID NO:6)
ATGGCGGCGGCGGCGGGGAATCGCGCCTCGTCGGGATTCCCGGGCGCCA
GGGCTA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising from about 10 to about 64 contiguous nucleotides from the nucleic acid sequence (SEQ ID NO:7)
GAGAAAATGGCGGCGGCGGCGGGGAATCGCGCCTCGTCGGGATTCCCGG
GCGCCAGGGCTA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:8) GCGCGCCCGCG and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:9) CCGCGAGCCGCGGCGGC and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

On page 24, please delete the subparagraphs at lines 10-30 and replace them with the following subparagraphs:

a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:10) TTTGGATGGTCA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:11) GGACAGCTTC and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:12) CCCCTGAGTGC and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

A³
a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:13) GCCAGCATTT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:14) CATCTAGACCT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:15) GGCTGTAGCA and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:16) GTAATGCTGT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

On page 25, please delete the subparagraph at lines 4-6 and replace it with the following subparagraph:

A⁴ a nucleic acid molecule comprising the nucleic acid sequence (SEQ ID NO:17) GGATGCCCTCCCCAT and having at least 80% homology to the nucleic acid sequence shown in SEQ ID NO:1;

On page 35, please delete the subparagraphs at lines 23-30 and replace them with the following subparagraphs:

A⁵ a polypeptide comprising from about 5 to about 19 contiguous amino acids from the amino acid sequence (SEQ ID NO:18) MAAAAGNRASSSGFPGARAT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising from about 5 to about 19 contiguous amino acids from the amino acid sequence (SEQ ID NO:19) EKMAAAAGNRASSSGFPGARAT and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

On page 36, please delete the subparagraphs at lines 1-24 and replace them with the following subparagraphs:

A⁶ a polypeptide comprising the amino acid sequence (SEQ ID NO:20) SAPAA and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:21) ASRGG and having at least 80% homology to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:22)
CARGT and having at least 80% homology to the amino acid sequence shown in
SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:23)
VSSSTH and having at least 80% homology to the amino acid sequence shown in
SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:24)
LMAIADE and having at least 80% homology to the amino acid sequence shown
in SEQ ID NO:2;

AG
a polypeptide comprising the amino acid sequence (SEQ ID NO:25)
TLDGQQDSFLQASVPNNYLETTENSSPECT and having at least 80% homology
to the amino acid sequence shown in SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:26)
LASISV and having at least 80% homology to the amino acid sequence shown in
SEQ ID NO:2;

a polypeptide comprising the amino acid sequence (SEQ ID NO:27)
SFGCSSNSSNAVIPSDE and having at least 80% homology to the amino acid
sequence shown in SEQ ID NO:2; or

a polypeptide comprising the amino acid sequence (SEQ ID NO:28)
SQDALPIVPQLQVENGEDIIIIQQDTPETLPGHTKAKQPYREDT and having at
least 80% homology to the amino acid sequence shown in SEQ ID NO:2.

Amendments to the Claims:

Please amend claims 3 and 10 as described below. As required by
37 C.F. R. § 1.121(b)(1), the amended claims are rewritten with the amended
claim language included. A marked-up version of the amended claims is
attached to show the changes relative to the as-filed version.